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SEQUENCE LISTING

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<120> METHOD FOR PRODUCING L-GLUTAMIC ACID BY FERMENTATION ACCOMPANIED BY
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<210> 1

<211> 4556

<212> DNA

<213> Enterobacter agglomerans

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Pro Ala Thr Asn Ser Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala				
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Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Cys Val Pro Ser	
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Ala Glu Glu Ala Ala Ser Lys Ile Gly Ala	
1415 1420	

<210> 2

<211> 39

<212> PRT

<213> Enterobacter agglomerans

<400> 2

Ala Phe Ser Val Phe Arg Cys His Ser Ile Met Asn Cys Val Ser Val	
1 5 10 15	
Cys Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His Ile Lys Ser	
20 25 30	

Met Leu Leu Gln Arg Ser Ala
35

<210> 3

<211> 935

<212> PRT

<213> Enterobacter agglomerans

<400> 3

Met Gln Asn Ser Ala Met Lys Pro Trp Leu Asp Ser Ser Trp Leu Ala
1 5 10 15

Gly Ala Asn Gln Ser Tyr Ile Glu Gln Leu Tyr Glu Asp Phe Leu Thr
20 25 30

Asp Pro Asp Ser Val Asp Ala Val Trp Arg Ser Met Phe Gln Gln Leu
35 40 45

Pro Gly Thr Gly Val Lys Pro Glu Gln Phe His Ser Ala Thr Arg Glu
50 55 60

Tyr Phe Arg Arg Leu Ala Lys Asp Ala Ser Arg Tyr Thr Ser Ser Val
65 70 75 80

Thr Asp Pro Ala Thr Asn Ser Lys Gln Val Lys Val Leu Gln Leu Ile
85 90 95

Asn Ala Phe Arg Phe Arg Gly His Gln Glu Ala Asn Leu Asp Pro Leu
100 105 110

Gly Leu Trp Lys Gln Asp Arg Val Ala Asp Leu Asp Pro Ala Phe His
115 120 125

Asp Leu Thr Asp Ala Asp Phe Gln Glu Ser Phe Asn Val Gly Ser Phe
 130 135 140

Ala Ile Gly Lys Glu Thr Met Lys Leu Ala Asp Leu Phe Asp Ala Leu
 145 150 155 160

Lys Gln Thr Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Ile Asn
 165 170 175

Asn Thr Glu Glu Lys Arg Trp Ile Gln Gln Arg Ile Glu Ser Gly Ala
 180 185 190

Ser Gln Thr Ser Phe Ser Gly Glu Glu Lys Lys Gly Phe Leu Lys Glu
 195 200 205

Leu Thr Ala Ala Glu Gly Leu Glu Lys Tyr Leu Gly Ala Lys Phe Pro
 210 215 220

Gly Ala Lys Arg Phe Ser Leu Glu Gly Gly Asp Ala Leu Val Pro Met
 225 230 235 240

Leu Arg Glu Met Ile Arg His Ala Gly Lys Ser Gly Thr Arg Glu Val
 245 250 255

Val Leu Gly Met Ala His Arg Gly Arg Leu Asn Val Leu Ile Asn Val
 260 265 270

Leu Gly Lys Lys Pro Gln Asp Leu Phe Asp Glu Phe Ser Gly Lys His
 275 280 285

Lys Glu His Leu Gly Thr Gly Asp Val Lys Tyr His Met Gly Phe Ser
 290 295 300

Ser Asp Ile Glu Thr Glu Gly Gly Leu Val His Leu Ala Leu Ala Phe
 305 310 315 320

Asn Pro Ser His Leu Glu Ile Val Ser Pro Val Val Met Gly Ser Val

325

330

335

Arg Ala Arg Leu Asp Arg Leu Ala Glu Pro Val Ser Asn Lys Val Leu
 340 345 350

Pro Ile Thr Ile His Gly Asp Ala Ala Val Ile Gly Gln Gly Val Val
 355 360 365

Gln Glu Thr Leu Asn Met Ser Gln Ala Arg Gly Tyr Glu Val Gly Gly
 370 375 380

Thr Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr Ser Asn
 385 390 395 400

Pro Lys Asp Ala Arg Ser Thr Pro Tyr Cys Thr Asp Ile Gly Lys Met
 405 410 415

Val Leu Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val
 420 425 430

Ala Phe Val Thr Arg Leu Ala Leu Asp Tyr Arg Asn Thr Phe Lys Arg
 435 440 445

Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu
 450 455 460

Ala Asp Glu Pro Ser Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys
 465 470 475 480

Lys His Pro Thr Pro Arg Lys Ile Tyr Ala Asp Arg Leu Glu Gly Glu
 485 490 495

Gly Val Ala Ser Gln Glu Asp Ala Thr Glu Met Val Asn Leu Tyr Arg
 500 505 510

Asp Ala Leu Asp Ala Gly Glu Cys Val Val Pro Glu Trp Arg Pro Met
 515 520 525

Ser Leu His Ser Phe Thr Trp Ser Pro Tyr Leu Asn His Glu Trp Asp
530 535 540

Glu Pro Tyr Pro Ala Gln Val Asp Met Lys Arg Leu Lys Glu Leu Ala
545 550 555 560

Leu Arg Ile Ser Gln Val Pro Glu Gln Ile Glu Val Gln Ser Arg Val
565 570 575

Ala Lys Ile Tyr Asn Asp Arg Lys Leu Met Ala Glu Gly Glu Lys Ala
580 585 590

Phe Asp Trp Gly Gly Ala Glu Asn Leu Ala Tyr Ala Thr Leu Val Asp
595 600 605

Glu Gly Ile Pro Val Arg Leu Ser Gly Glu Asp Ser Gly Arg Gly Thr
610 615 620

Phe Phe His Arg His Ala Val Val His Asn Gln Ala Asn Gly Ser Thr
625 630 635 640

Tyr Thr Pro Leu His His Ile His Asn Ser Gln Gly Glu Phe Lys Val
645 650 655

Trp Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly
660 665 670

Tyr Ala Thr Ala Glu Pro Arg Val Leu Thr Ile Trp Glu Ala Gln Phe
675 680 685

Gly Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser
690 695 700

Ser Gly Glu Gln Lys Trp Gly Arg Met Cys Gly Leu Val Met Leu Leu
705 710 715 720

Pro His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu
725 730 735

Glu Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Cys Val
740 745 750

Pro Ser Thr Pro Ala Gln Val Tyr His Met Leu Arg Arg Gln Ala Leu
755 760 765

Arg Gly Met Arg Arg Pro Leu Val Val Met Ser Pro Lys Ser Leu Leu
770 775 780

Arg His Pro Leu Ala Ile Ser Ser Leu Asp Glu Leu Ala Asn Gly Ser
785 790 795 800

Phe Gln Pro Ala Ile Gly Glu Ile Asp Asp Leu Asp Pro Gln Gly Val
805 810 815

Lys Arg Val Val Leu Cys Ser Gly Lys Val Tyr Tyr Asp Leu Leu Glu
820 825 830

Gln Arg Arg Lys Asp Glu Lys Thr Asp Val Ala Ile Val Arg Ile Glu
835 840 845

Gln Leu Tyr Pro Phe Pro His Gln Ala Val Gln Glu Ala Leu Lys Ala
850 855 860

Tyr Ser His Val Gln Asp Phe Val Trp Cys Gln Glu Glu Pro Leu Asn
865 870 875 880

Gln Gly Ala Trp Tyr Cys Ser Gln His His Phe Arg Asp Val Val Pro
885 890 895

Phe Gly Ala Thr Leu Arg Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro
900 905 910

Ala Val Gly Tyr Met Ser Val His Gln Gln Gln Gln Gln Asp Leu Val

915

920

925

Asn Asp Ala Leu Asn Val Asn
930 935

<210> 4

<211> 407

<212> PRT

<213> Enterobacter agglomerans

<400> 4

Met Ser Ser Val Asp Ile Leu Val Pro Asp Leu Pro Glu Ser Val Ala
1 5 10 15

Asp Ala Thr Val Ala Thr Trp His Lys Lys Pro Gly Asp Ala Val Ser
20 25 30

Arg Asp Glu Val Ile Val Glu Ile Glu Thr Asp Lys Val Val Leu Glu
35 40 45

Val Pro Ala Ser Ala Asp Gly Val Leu Glu Ala Val Leu Glu Asp Glu
50 55 60

Gly Ala Thr Val Thr Ser Arg Gln Ile Leu Gly Arg Leu Lys Glu Gly
65 70 75 80

Asn Ser Ala Gly Lys Glu Ser Ser Ala Lys Ala Glu Ser Asn Asp Thr
85 90 95

Thr Pro Ala Gln Arg Gln Thr Ala Ser Leu Glu Glu Glu Ser Ser Asp
100 105 110

Ala Leu Ser Pro Ala Ile Arg Arg Leu Ile Ala Glu His Asn Leu Asp
115 120 125

Ala Ala Gln Ile Lys Gly Thr Gly Val Gly Gly Arg Leu Thr Arg Glu
 130 135 140

Asp Val Glu Lys His Leu Ala Asn Lys Pro Gln Ala Glu Lys Ala Ala
 145 150 155 160

Ala Pro Ala Ala Gly Ala Ala Thr Ala Gln Gln Pro Val Ala Asn Arg
 165 170 175

Ser Glu Lys Arg Val Pro Met Thr Arg Leu Arg Lys Arg Val Ala Glu
 180 185 190

Arg Leu Leu Glu Ala Lys Asn Ser Thr Ala Met Leu Thr Thr Phe Asn
 195 200 205

Glu Ile Asn Met Lys Pro Ile Met Asp Leu Arg Lys Gln Tyr Gly Asp
 210 215 220

Ala Phe Glu Lys Arg His Gly Val Arg Leu Gly Phe Met Ser Phe Tyr
 225 230 235 240

Ile Lys Ala Val Val Glu Ala Leu Lys Arg Tyr Pro Glu Val Asn Ala
 245 250 255

Ser Ile Asp Gly Glu Asp Val Val Tyr His Asn Tyr Phe Asp Val Ser
 260 265 270

Ile Ala Val Ser Thr Pro Arg Gly Leu Val Thr Pro Val Leu Arg Asp
 275 280 285

Val Asp Ala Leu Ser Met Ala Asp Ile Glu Lys Lys Ile Lys Glu Leu
 290 295 300

Ala Val Lys Gly Arg Asp Gly Lys Leu Thr Val Asp Asp Leu Thr Gly
 305 310 315 320

Gly Asn Phe Thr Ile Thr Asn Gly Gly Val Phe Gly Ser Leu Met Ser
325 330 335

Thr Pro Ile Ile Asn Pro Pro Gln Ser Ala Ile Leu Gly Met His Ala
340 345 350

Ile Lys Asp Arg Pro Met Ala Val Asn Gly Gln Val Val Ile Leu Pro
355 360 365

Met Met Tyr Leu Ala Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Arg
370 375 380

Glu Ser Val Gly Tyr Leu Val Ala Val Lys Glu Met Leu Glu Asp Pro
385 390 395 400

Ala Arg Leu Leu Leu Asp Val
405

<210> 5

<211> 40

<212> PRT

<213> Enterobacter agglomerans

<400> 5

Met Asn Leu His Glu Tyr Gln Ala Lys Gln Leu Phe Ala Arg Tyr Gly
1 5 10 15

Met Pro Ala Pro Thr Gly Tyr Ala Cys Thr Thr Pro Arg Glu Ala Glu
20 25 30

Glu Ala Ala Ser Lys Ile Gly Ala
35 40

<210> 6

<211> 30

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Artificial Sequence: synthetic DNA

<400> 6

gtcgacaata gccygaatct gttctggtcg

30

<210> 7

<211> 30

<212> DNA

<213> Artibeus anderseni

<220>

<221> misc_feature

<222> ()..()

<223> Artificial Sequence: synthetic DNA

<400> 7

aagcttatcg acgctcccct cccacacggt

30